

3

RECEIVED

JUN 26 2001

TECH CENTER 1600 2000

SEQUENCE LISTING



(1) GENERAL INFORMATION:

- (i) APPLICANT: Cassels, Frederick J.  
Loomis-Price, Lawrence
- (ii) TITLE OF INVENTION: PEPTIDES FROM A CONSENSUS PEPTIDE OF  
E. COLI CS4-CFA/I FAMILY PROTEINS
- (iii) NUMBER OF SEQUENCES: 37
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Hendricks and Assoc.
  - (B) STREET: P.O. Box 2509
  - (C) CITY: Fairfax
  - (D) STATE: VA
  - (E) COUNTRY: US
  - (F) ZIP: 22031
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/905,140
  - (B) FILING DATE: 01-SEP-1997
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Hendricks, Glenna M.
  - (B) REGISTRATION NUMBER: 32.535
  - (C) REFERENCE/DOCKET NUMBER: cas905
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (703) 591-4470
  - (B) TELEFAX: (702) 591-4428

*Sub  
vi*

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: E. coli
- (B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala	Ser	Val	Asp	Pro	Thr	Ile	Asp	Leu	Leu	Gln	Ala
1				5					10		

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: E. coli
- (B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ala	Ser	Val	Asp	Pro	Thr	Ile	Asp	Leu	Leu	Gln	Ala
1				5					10		

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: E. coli
- (B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp Thr Val Thr Ala Ser Val Asp Pro Thr Ile Asp Leu Leu Gln Ala  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

*sub*  
*u*  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: E. coli  
(B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Val Thr Ala Ser Val Asp Pro Thr Ile Asp Leu Leu Gln Ala Asp  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: E. coli  
(B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Thr Ala Ser Val Asp Pro Thr Ile Asp Leu Leu Gln Ala Asp

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 13 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: E. coli  
    (B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Thr Ala Ser Val Asp Pro Thr Ile Asp Leu Leu Gln Ala  
1                    5                    10

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 8 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: E. coli  
    (B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Val Glu Lys Asn Ile Thr Val Thr  
1                    5

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 8 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: E. coli
- (B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Glu Lys Asn Ile Thr Val Thr Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: E. coli
- (B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Lys Asn Ile Thr Val Thr Ala Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: E. coli

(B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asn Ile Thr Val Thr Ala Ser Val  
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: E. coli

(B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ile Thr Val Thr Ala Ser Val Asp  
1 5

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: E. coli

(B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Thr Val Thr Ala Ser Val Asp Pro  
1 5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: E. coli  
(B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Val Thr Ala Ser Val Asp Pro Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: E. coli  
(B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Thr Ala Ser Val Asp Pro Thr Ile

1

5

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 8 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: E. coli  
    (B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

*auth*  
*(u)*  
Ala Ser Val Asp Pro Thr Ile Asp  
1                                    5

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 8 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: E. coli  
    (B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser Val Asp Pro Thr Ile Asp Leu  
1                                    5

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 8 amino acids



- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: E. coli
- (B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Val Asp Pro Thr Ile Asp Leu Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

*sub*  
*seq*  
(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: E. coli
- (B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Asp Pro Thr Ile Asp Leu Leu Gln  
1 5

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: E. coli

(B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Pro Thr Ile Asp Leu Leu Gln Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

*Just a*  
(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: E. coli

(B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Thr Ile Asp Leu Leu Gln Ala Asp  
1 5

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: E. coli

(B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ile Asp Leu Leu Gln Ala Asp Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: E. coli
- (B) STRAIN: CS4-CFA/I

*Sub 213*  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Asp Leu Leu Gln Ala Asp Gly Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: E. coli
- (B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Leu Leu Gln Ala Asp Gly Ser Ala

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 8 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: E. coli  
    (B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Leu Gln Ala Asp Gly Ser Ala Leu  
1                    5

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 8 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: E. coli  
    (B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Gln Ala Asp Gly Ser Ala Leu Pro  
1                    5

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 8 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: E. coli
- (B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ala Asp Gly Ser Ala Leu Pro Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: E. coli
- (B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Asp Gly Ser Ala Leu Pro Ser Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: E. coli

(B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Gly Ser Ala Leu Pro Ser Ala Val  
1 5

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: E. coli

(B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Ser Ala Leu Pro Ser Ala Val Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: E. coli

(B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ala Leu Pro Ser Ala Val Ala Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: E. coli  
(B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Leu Pro Ser Ala Val Ala Leu Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: E. coli  
(B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Pro Ser Ala Val Ala Leu Thr Tyr

1

5

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 8 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: E. coli  
    (B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ser Ala Val Ala Leu Thr Tyr Ser  
1                                    5

(2) INFORMATION FOR SEQ ID NO:34:

- Sent to Ci*
- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 8 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: E. coli  
    (B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ala Val Ala Leu Thr Tyr Ser Pro  
1                                    5

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 8 amino acids



- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: E. coli
- (B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Val Ala Leu Thr Tyr Ser Pro Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: E. coli
- (B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Pro Ser Ala Val Ala Leu Thr Tyr Ser Pro  
1 5 10

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: E. coli

(B) STRAIN: CS4-CFA/I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

*Sub*  
*vi* Ile Cys Val Glu Lys Asn Ile Thr Val Thr Ala Ser Val Asp Pro Thr  
1 5 10 15

Leu Asp Leu Leu Gln Ala Asp Gly Ser Ala Leu Pro Ser Ala Val Ala  
20 25 30

Thr Tyr Ser Pro Ala  
35